IN THE TITLE:

Please amend the title as follows:

"METHOD OF HANDLING DATAB<u>A</u>SE FOR BIOINFORMATICS"

IN THE SPECIFICATION:

Please amend the specification as follows:

Beginning on page 1, line 19 running to page 2, line 4, delete the existing paragraph

entitled "Description of the background" and replace with the following:

--Description of the background

Successful achievement of human gene projects performed in the early twenty-first

century brought about rapid development in all life science fields. Due to completion of the

human gene map, studies on ~~the~~ human genes and the structures and functions of human proteins

will be actively carried out ~~in~~ post genome ~~genom~~. While a computer stores information

represented by 0 and 1, ~~the~~ human genes store ~~stores~~ information of about three billion ~~billions~~

represented by four letters, A, T, G and C. As the studies are performed, a vast amount of digital

information is being accumulated and many databases related with bioinformatics, such as

SwissProt, GenBank® ~~GenBank~~ and the European Molecular Biology Laboratory (EMBL)

~~EMBL~~, are opened to the public through a web.--

Beginning on page 2, line 5 running through line 9, please delete the existing first

paragraph and replace it with the following:

--There are various programs used for searching these bioinformatics databases for

appropriate gene information at the request of a user. These programs are classified into a

pattern match program (such as ~~FastA, BLAST~~ FASTA™, BLAST™ (Basic Local Alignment

Search Tool), and CLUSTALW™ ~~Clustal W~~, which search ~~searches~~ for data composed of A, T,

G and C to perform sequence comparison) [,] and a program of predicting a structure from data

sequence [,] (such as <u>J-NET™ and J-PRED™</u> ~~J-NET and J-PRED~~).--

Beginning on page 2, line 17 running through page 3 (renumbered) line 3, please delete

the last paragraph and replace it by the following:

--The programs such as <u>FASTA™ and BLAST™</u> ~~FastA and BLAST~~ are provided to

users through a web. A user connects to a server to transmit a protein sequence he/she wants to

compare and analyze to the server. Then, the server reads sequences from the database and

compares them with the protein sequence requested by the user. These programs operate based

on a database. That is, the programs should access the database to read data and respond to a

user's request for every user request. In case of <u>FASTA™</u> ~~FastA~~, for instance, a user transmits a

sequence he/she wants to compare/analyze to <u>FASTA™</u> ~~FastA~~ server. The transmitted sequence

is compared with sequences stored in the database to check similarity, and sequences having

similarity of higher than a predetermined value are returned to the user. Here, the server

accesses the database for each user's request.—

Beginning on page 4 (renumbered), line 8 running through line 11, please delete the

existing paragraph and replace it with the following:

--The average time taken for one user to connect to the server and compare one <u>sequence</u>

~~sequences~~ with the sequences of the database, C_{avg}^0, which corresponds to the sum of the time of

equation (a) and the time of equation (2), can be represented as follows.

$$C_{avg}^0 = C_{DB} + C_{seq} = C_{io}N_b + C_{cpu}N_b = \left(C_{io} + C_{cpu}\right)N_b \text{--}$$

Beginning on page 5 (renumbered), line 10 running through line 16, please delete the

existing paragraph and replace it with the following:

--Accordingly, the present invention has been made in view of the above problems, and it is an object of the present invention ~~is~~ to provide a database handling a method in which, when a user requests the database server to process comparison of a bioinformatics-related sequence, the server does not wait for completion of processing of a previous user request being processed but processes the new user request and the previous user request simultaneously, so that the server can access the database only once for each user request, thereby saving system cost and response time.--

Beginning on page 8 (renumbered), line 11 running through line 15, please delete the existing paragraph and replace it with the following:

--In the meantime ~~mean time~~, the sequence comparison/analysis program 3-2 initializes a specific parameter k to set in association with the operation thereof. At step S21, when there is a user-requested sequence in the queue, the sequence comparison/analysis program 3-2 reads the kth sequence from the database 4 at step S22, and then compares it with all of sequences stored in the queue at step S23 (Third stage).--

Beginning on page 9 (renumbered), line 1 running through line 5, please delete the existing paragraph and replace it with the following:

--As described above, the present invention <u>simultaneously</u> processes <u>the</u> currently requested sequence and the <u>previously</u> ~~previous~~ requested sequence ~~being processed,~~ ~~simultaneously~~. This is possible because all of <u>the</u> data of the database can be processed irrespective of <u>the</u> data processing order since all of <u>the</u> sequences of the database are generally

searched in sequence search of bioinformatics and there is no dependence among the data items

of the bioinformatics database.--

Beginning on page 12 (renumbered), line 14 running through line 20, please delete the

existing paragraph and replace it with the following:

--The database GenBank® ~~GenBank~~ (Protein Sequence Database of Rip International

Release 72.02), actually being used in bioinformatics, was managed by Los ~~Ros~~ Alamos research

institute in support of National Institute of Health in 1981, and transferred to National Center for

Biotechnology Information (NCBI) under the control of National Library of Medicine in 1992.

With this GenBank® ~~GenBank~~, cytochrome that acts upon oxidization and reduction of cells,

one of human proteins, was used as a user-requested sequence. As a result, C_{DB} was 3.99sec and

C_{seq}, the cost required for comparing the user-requested sequence with all of sequences of the

database, was 19.98 sec.--